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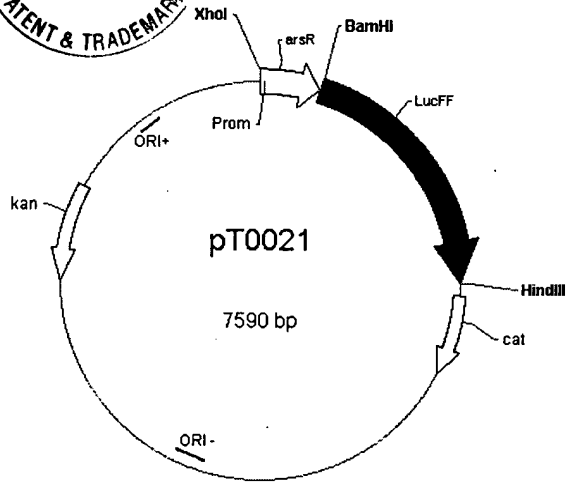
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**Figure 1A**



**HA  
tag**

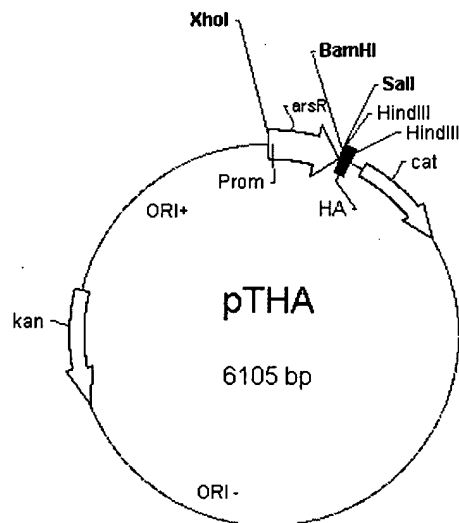
*Bam*HI      *Sal*I      *Hind*III      stop

GATCCCGGTCGACCAAGCTTTACCCATACGACGTCCCAGACTACGCCAGCTGA  
GGCCAGCTGGTTCGAAATGGGTATGCTGCAGGGTCTGATGCGGTCGACTTCGA

*Hind*III

### Digestion with *Bam*HI and *Hind*III

## Ligation





**Figure 1B**

PCR of pT0021 with XhoI and BamHNR

XhoI-5'-AATTCTCGAGTAAAATAACAT-3  
XhoI

AAATCAGGTGACTGTTGAGAAAAGGAGGCGGATCCCG-BamHNR  
Stop of  
arsR                      RBS                      BamHI

Digestion with XhoI and BamHI

Ligation

PCR of pT0021 with LucFFB and LucFFH

LucFFB-5'-CGGGATCCATGAGGGGTTCCGAAGACG  
BamHI                      Start                      Original BamHI  
   of LucFF                      was modified

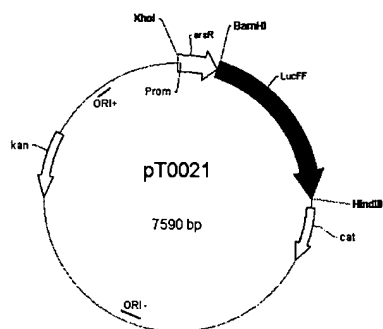
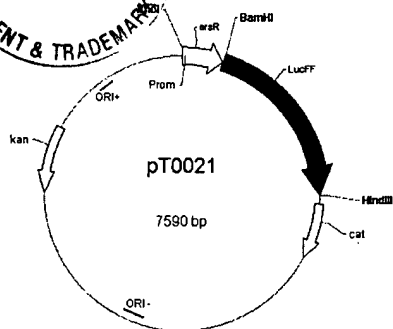
GAAAGTCCAAATTGTAAGCTTGGG-LucFFH  
Stop of                      HindIII  
LucFF

Digestion with BamHI and HindIII

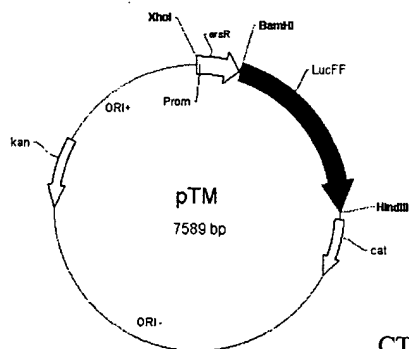
Ligation

- Modified in the vicinity of BamHI
- Cloning site for ORFs: BamHI and HindIII
- No additional codons in the induced protein

Prom                      arsR                      LucFF  
CTCGAG-----ATG-----TGAGAAAAGGAGGCGGATCCATG-----TAAGCTT  
XhoI                      RBS                      BamHI                      HindIII



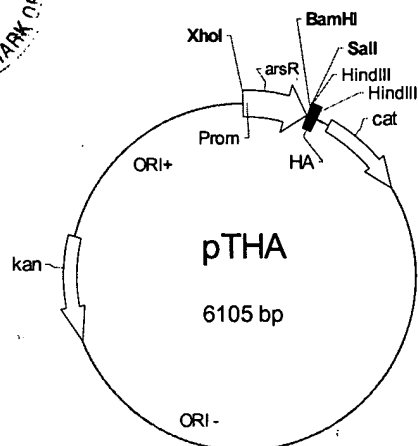
Modified between stop  
of arsR to BamHI



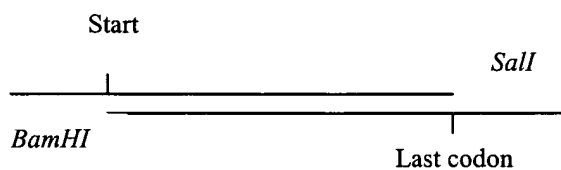




**Figure 2A**

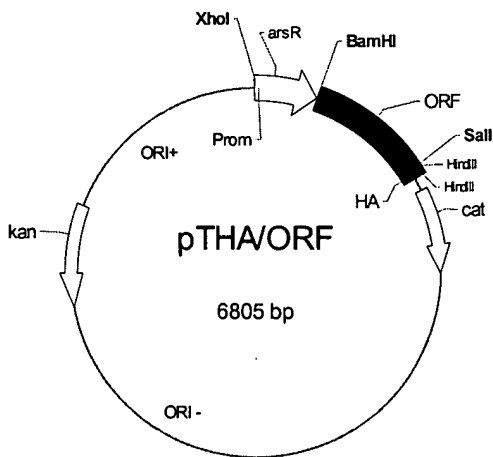


PCR of phage DNA with  
ORF specific primers



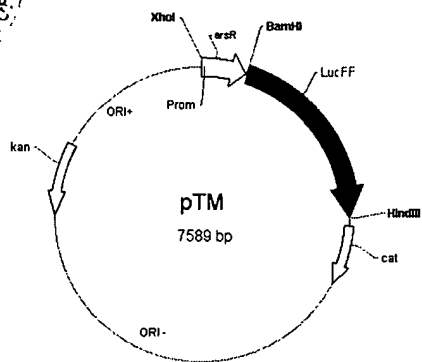
Digestion with *BamHI* and *Sall*

Ligation

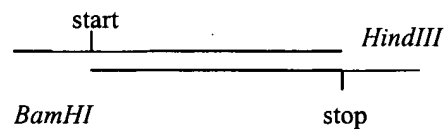




**Figure 2B**

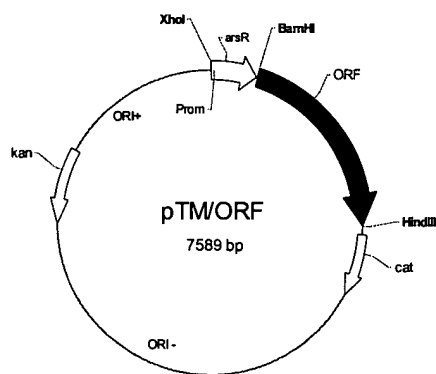


PCR of phage DNA with  
ORF specific primers



Digestion with *Bam*HI and *Hind*III

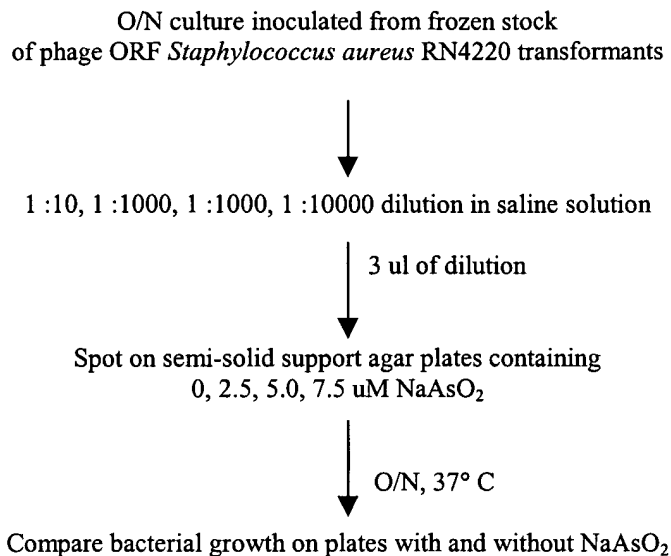
Ligation



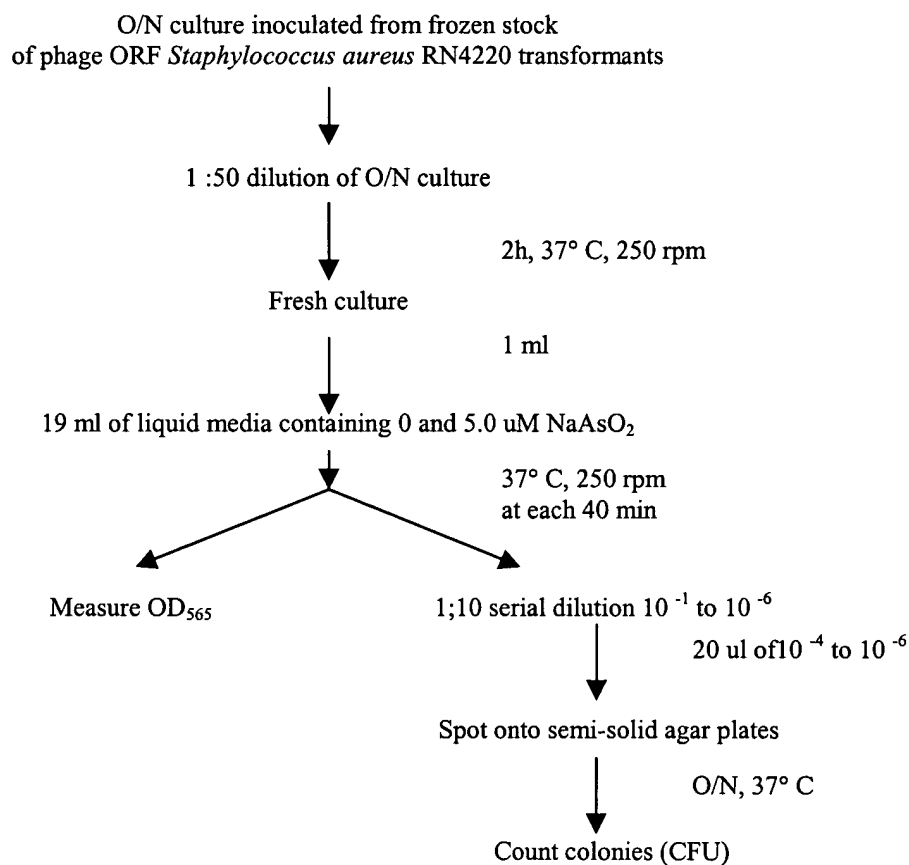


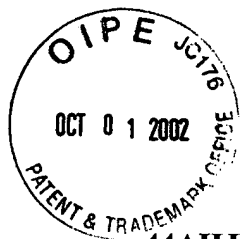
**Figure 3**

**3A: Functional assay on semi-solid support medium**



**3B: Functional assay in liquid medium**





**Figure 4A**

**44AHJD ORFs tested for functional analysis**

UID	POS
44AHJDORF001	12627..10342
44AHJDORF002	3789..5732
44AHJDORF003	6626..8389
44AHJDORF004	8764..10227
44AHJDORF005	13890..12643
44AHJDORF006	803..2029
44AHJDORF007	2044..3027
44AHJDORF008	3020..3775
44AHJDORF009	5744..6496
44AHJDORF010	14420..13938
44AHJDORF011	15593..15225
44AHJDORF012	8391..8813
44AHJDORF013	14996..14586
44AHJDORF019	9836..9630
44AHJDORF023	6494..6315
44AHJDORF025	15175..14999
44AHJDORF027	12916..13080
44AHJDORF028	9235..9071
44AHJDORF035	13957..13811
44AHJDORF036	10165..10019
44AHJDORF039	1743..1883
44AHJDORF040	9740..9877
44AHJDORF044	12917..12783
44AHJDORF046	4891..5019
44AHJDORF048	15340..15212
44AHJDORF049	5784..5909
44AHJDORF053	3348..3467
44AHJDORF113	199..600
44AHJDORF114	16172..15870
44AHJDORF121	16362..16165
44AHJDORF123	614..796



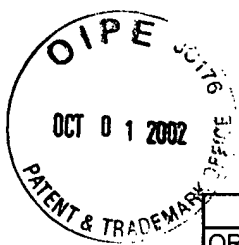


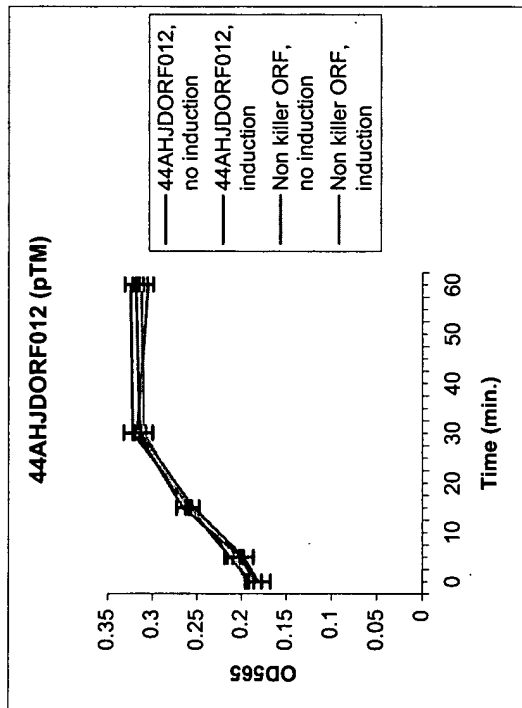
Figure 4B

ORF ID	<i>Staphylococcus aureus</i> transformants	Semi-solid support media		
		Without induction		With induction (5 uM sodium arsenite)
44AHJDORF12	Clone1			
	Clone2			
	Clone3			
44AHJDORF25	Clone1			
	Clone2			
	Clone3			
Control 77ORF30	Clone1			



Figure 5A

Frame 1



Frame 2

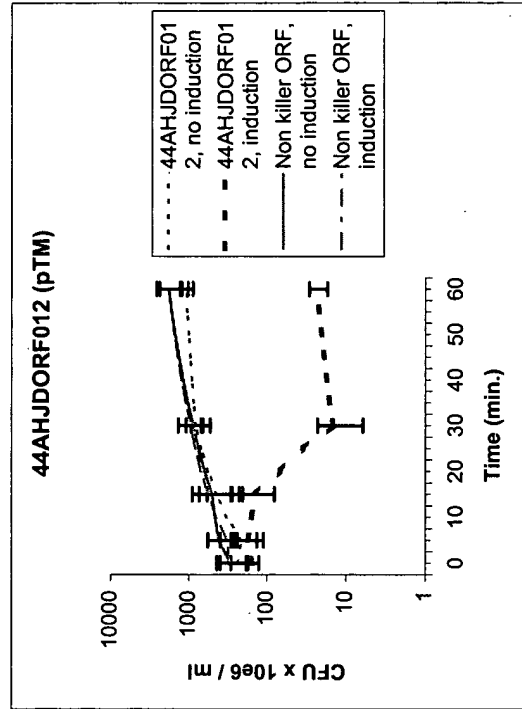
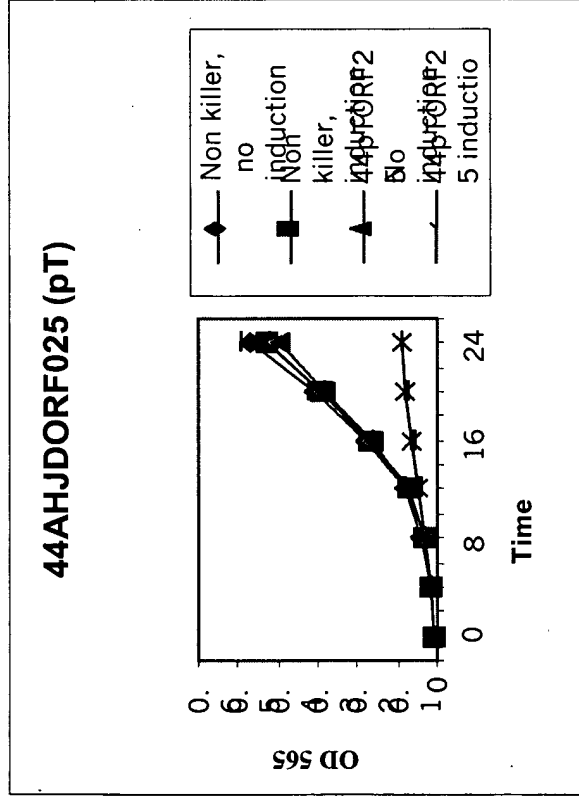
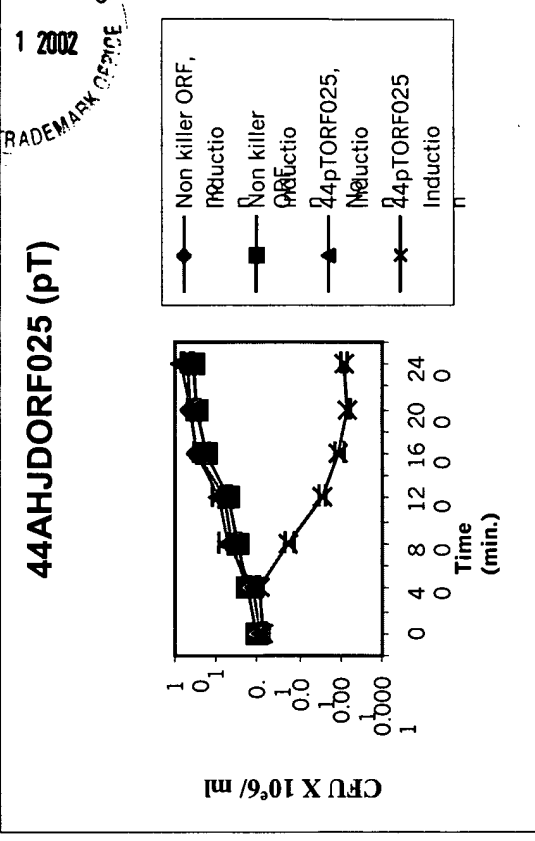


Figure 5B

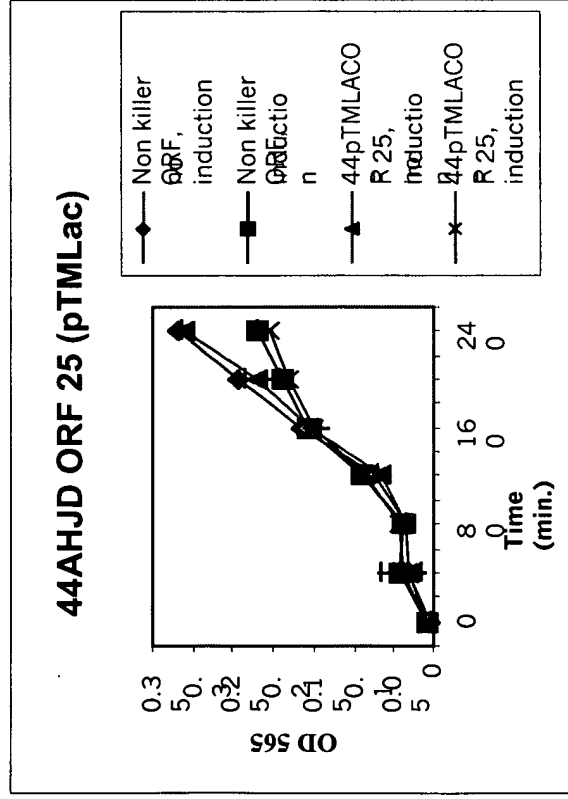
Frame 1



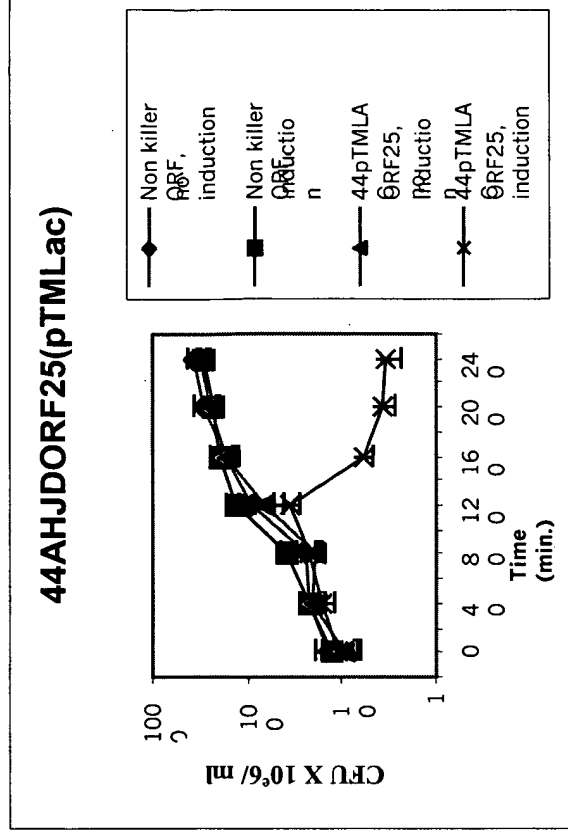
Frame 2



Frame 3



Frame 4





**FIGURE 6**

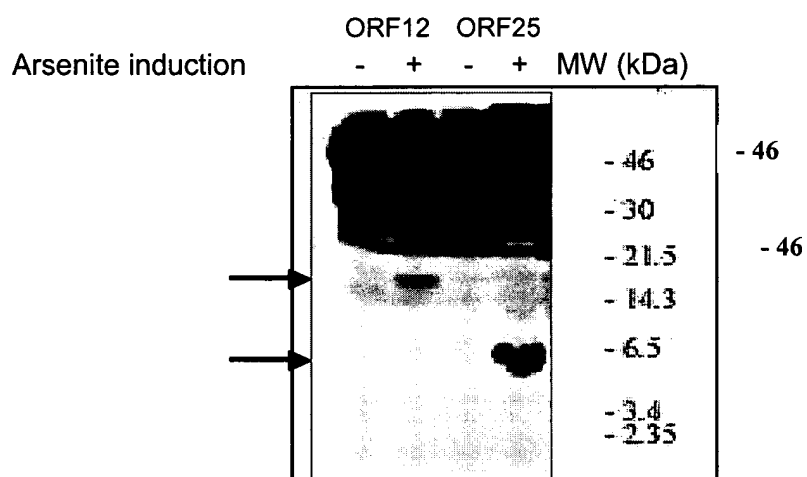
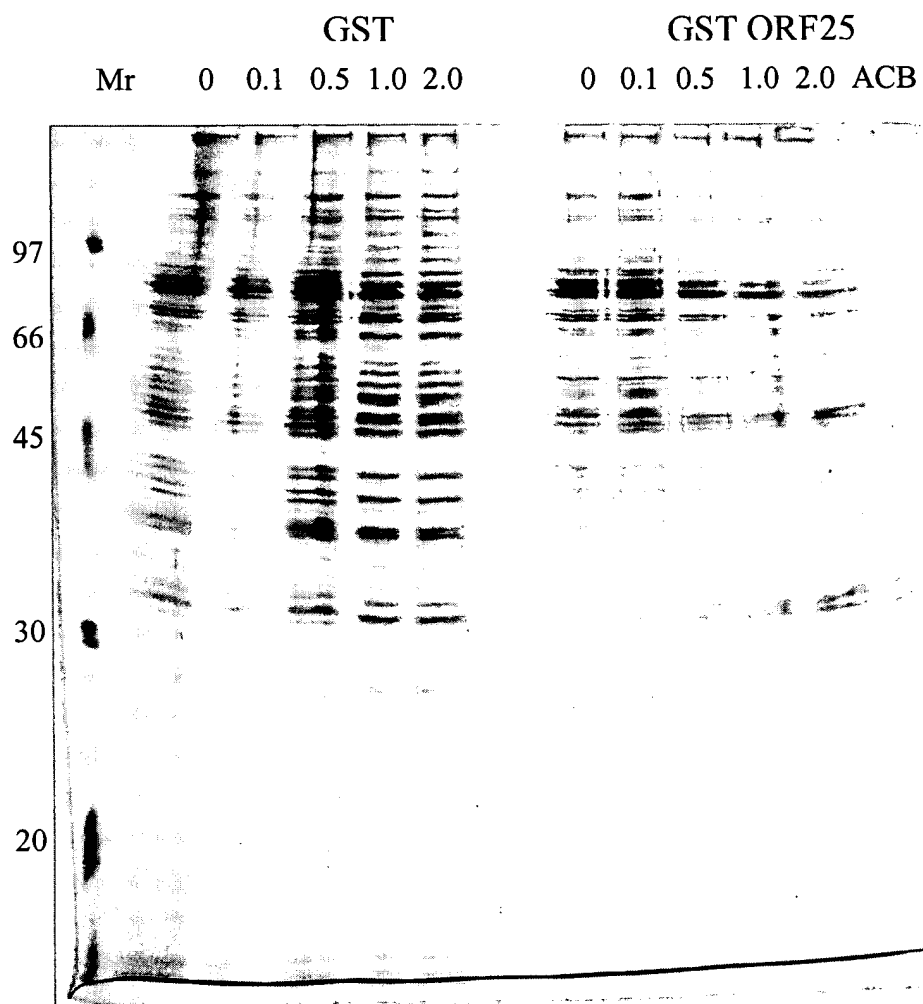
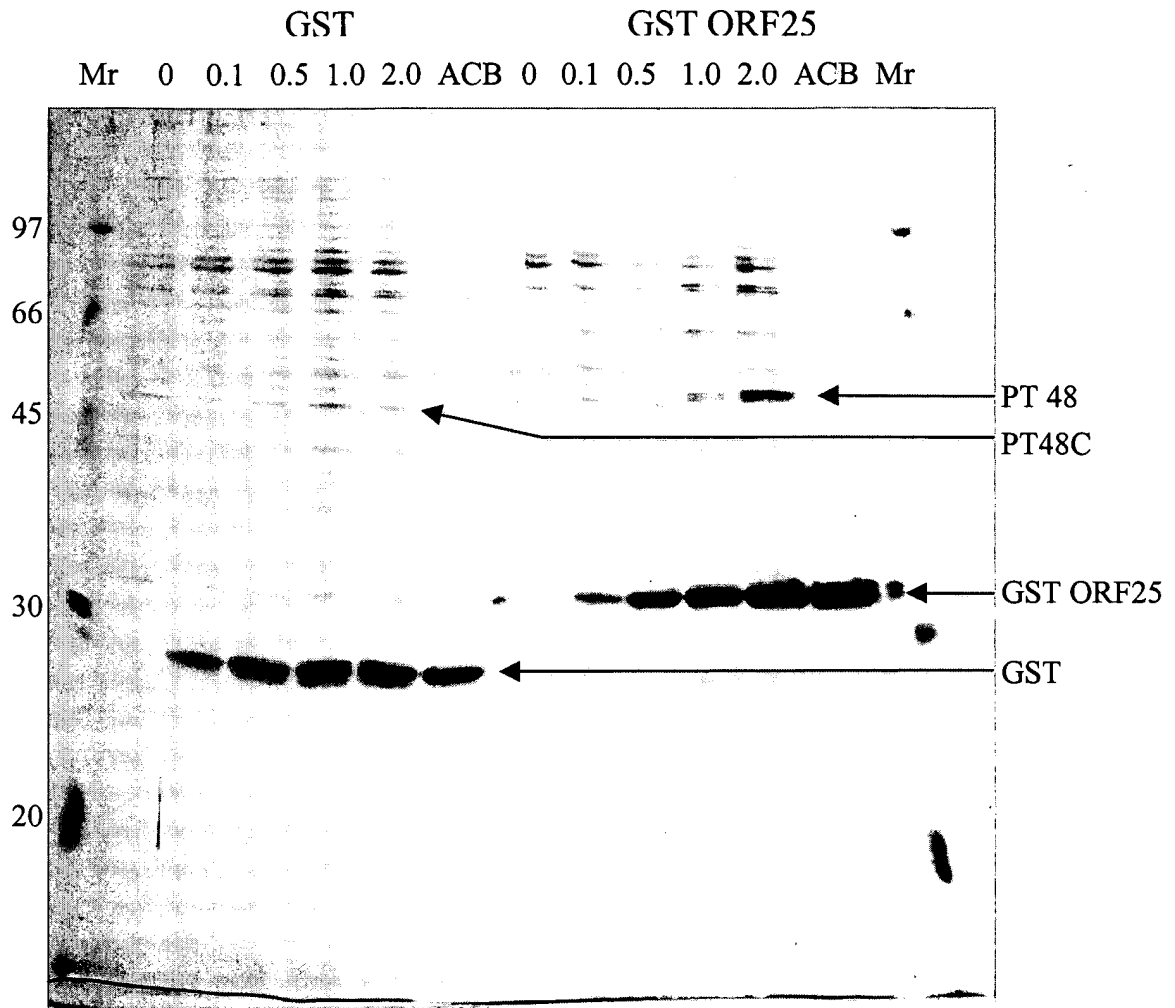




FIGURE 7A



**FIGURE 7B**



IR spectrum showing transmittance versus wavenumber (cm⁻¹). The x-axis ranges from 4000 to 500 cm⁻¹, and the y-axis ranges from 0 to 3000 transmittance units. The spectrum shows several characteristic absorption bands, including a broad peak around 3400 cm⁻¹, sharp peaks in the 1600-1700 cm⁻¹ region, and multiple peaks in the fingerprint region below 1500 cm⁻¹.

Wavenumber (cm⁻¹)
3677.5156
3671.3659
3089.401838
3005.5019
2966.6235
1666.6200
1640.5542
1552.5618
1516.5767
1502.6729
1428.6476
1301.6288
1402.6931
1478.7465
1426.7681
1400.7275
1392.6841
1316.7985
1317.7959
1324.6800
1256.8164
1642.6802
1649.7088
1703.9201
1752.9374
1768.8260
1782.6508
1788.9917
1831.9897
1875.9653
1990.0311
2006.9065
2170.3665
2165.0499
2157.1231
2165.0696
2273.2149
2289.0727
2291.1559
2310.2167
2321.1956
2368.1969
2475.1521
2667.2504
2701.2643



**FIGURE 9**

Details for : PT48

gil1706496|sp|P50029|DP3B\_STAAU DNA POLYMERASE III, BETA CHAIN

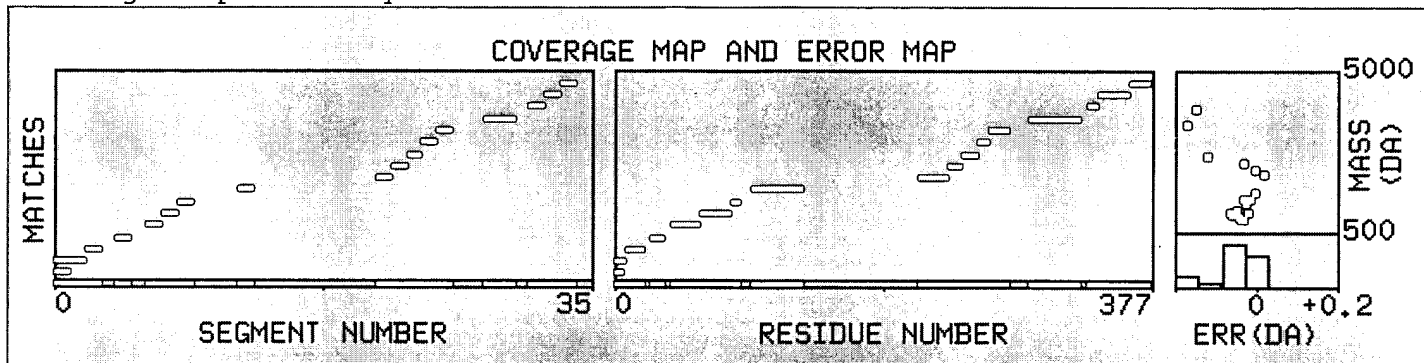
gil1084187|pir||S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Staphylococcus aureus

Sample ID : PT 48

Number of Measured Peptides : 40

Number of Matched Peptides : 17

Coverage of protein sequence : 68%



Measured Mass(M)	Avg/ Mono	Computed Mass	Error (Da)	Residues Start	To	Missed Cut	Peptide sequence
870.370	M	870.397	-0.027	333	339	0	YMDALK
880.474	M	880.505	-0.032	82	88	0	FFVDIIK
898.392	M	898.429	-0.037	1	7	0	MMEFTIK
1004.492	M	1004.540	-0.048	235	243	0	VGNVNFISR
1054.514	M	1054.530	-0.016	1	8	1	MMEFTIKR
1055.603	M	1055.658	-0.055	26	35	0	TTLPILTGIK
1151.546	M	1151.586	-0.040	255	263	0	LFPENYEIK
1300.619	M	1300.641	-0.021	244	254	0	LLEGHYPDTTR
1425.769	M	1425.782	-0.013	363	375	0	GDDSVTQLILPIR
1469.713	M	1469.740	-0.026	9	20	0	DYFITQLNDTLK
1648.781	M	1648.784	-0.003	264	277	0	LSIDNGEFYHAIDR
2156.112	M	2156.095	0.017	61	81	0	TVDGEDIVNISETGSVVLPGR
2309.198	M	2309.199	-0.000	40	60	0	EHEVILTGSDSEISIEITIPK
2474.139	M	2474.166	-0.027	214	234	0	IMSDNEEDIDIFFASNQVLFK
2666.266	M	2666.365	-0.099	340	362	0	AIDNDEVEVEFFGTMKPFILKPK
3577.670	A	3577.809	-0.139	292	326	1	LSTGDDVVELSSTSPEIGTVKEEVDANDVEGGSLK
4033.298	A	4033.421	-0.123	97	132	0	LSTNEQFQTLITSGHSEFNLSGLDPDQYPLLPQVSR





## FIGURE 10

**Figure 10A : SEQ ID NO : 166**

ATGATGGAATTCACTATTAAAAGAGATTATTTTATTACACAATTAAATGACACATTAAAA  
GCTATTTTACCAAGAACAACATTACCTATATTAACCTGGTATCAAAATCGATGCGAAAGAA  
CATGAAGTTATATTAACCTGGTTCAGACTCTGAAATTTCAATAGAAATCACTATTCCTAAA  
ACTGTAGATGGCGAAGATATTGTCAATATTTTCAGAAACAGGCTCAGTAGTACTTCCTGGA  
CGATTCTTTGTTGATATTATAAAAAAATTACCTGGTAAAGATGTTAAATTATCTACAAAT  
GAACAATTCCAGACATTAATTACATCAGGTCATTCTGAATTTAATTTAAGTGGCTTAGAT  
CCAGATCAATATCCTTTATTACCTCAAGTTTCTAGAGATGACGCAATTCAATTGTCGGTA  
AAAGTGCTTAAAAACGTGATTGCACAAACAAATTTTGCAGTGTCCACCTCAGAAACACGC  
CCAGTACTAACTGGTGTGAAGTGGCTTATACAAGAAAATGAATTAATATGCACAGCGACT  
GACTCACACCGCTTGGCTGTAAGAAAGTTGCAGTTAGAAGATGTTTCTGAAAAACAAAAAT  
GTCATCATTCCAGGTAAGGCTTTAGCTGAATTAAATAAAATTATGTCTGACAATGAAGAA  
GACATTGATATCTTCTTTGCTTCAAACCAAGTTTTATTTAAAGTTGGAAATGTGAACTTT  
ATTTCTCGATTATTAGAAGGACATTATCCTGATACAACACGTTTATTCCCTGAAAACTAT  
GAAATTAATTAAGTATAGACAATGGGGAGTTTTATCATGCGATTGATCGTGCCTCTTTA  
TTAGCGCGTGAAGGTGGTAATAACGTTATTAATTAAGTACAGGTGATGACGTTGTTGAA  
TTGTCTTCTACATCACCAGAAATTGGTACTGTAAAAGAAGAAGTTGATGCAAACGATGTT  
GAAGGTGGTAGCCTGAAAATTCATTCAACTCTAAATATATGATGGATGCTTTAAAGCA  
ATCGATAATGATGAGGTTGAAGTTGAATTCCTCGGTACAATGAAACCATTTATTCTAAAA  
CCAAAAGGTGACGACTCGGTAACGCAATTAATTTTACCAATCAGAACTTACTAA

**Figure 10B : SEQ ID NO : 167**

>gi|1084187|pir||S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain -  
Staphylococcus aureus

MMEFTIKRDYFITQLNDTLKAISPRITLPILTGIKIDAKEHEVILTGSDSEISIEITIPKTVGDGDIVNI  
SETGSVVLPGRFFVDIIKKLPKGDVKLSTNEQFQTLITSGHSEFNLSGLDPDQYPLLQVSRDDAIQLSV  
KVLKNVIAQTNFAVSTSETRPVLTVGNWLIQENELICTATDSHRLAVRKLQLEDVSENKNV IIPGKALAE  
LNKIMSDNEEDIDIFFASNQVLFKVGNVNFISRLLLEGHYPDTTRLFPENYEIKLSIDNGEFYHAIDRASL  
LAREGGNNVIKLS TGDDVVELSSTSPEIGTVKEEVDANDVEGGSLKISFNSKYMDALK AIDNDEVEVEF  
FGTMKPFILKPKGDDSVTQLILPIRTY